

<110> Edwin L. Madison
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Corvas International, Inc.

<120> NUCLEIC ACID MOLECULES ENCODING
TRANSMEMBRANE SERINE PROTEASES, THE ENCODED PROTEINS AND
METHODS BASED THEREON

<140> 09/000,000

<141> 2001-02-01

<150> 60/213,124

<151> 2000-06-22

<150> 60/234,840

<151> 2000-06-22

<150> 60/179,982

<151> 2000-02-03

<150> 60/183,542

<151> 2000-02-18

<150> 09/657,968

<151> 2000-02-08

<160> 72

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$\langle 211 \rangle$ 3147

<212> DN

<213> Homo Sapien

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<223> Nucleotide encoding MTSP1

<221> CDS

<222> (23) . . . (2589)

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<301> O'Brien, T.J. and Tanimoto, H.

<308> GenBank AR081724

<310> US Pat 5972616

<311> 1998-02-20

<312> 1999-10-26

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Gly Gly Pro Lys Asp Phe Gly Ala Gly Leu Lys Tyr Asn Ser Arg His

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Glu Lys Val Asn Gly Leu Glu Glu Gly Val Glu Phe Leu Pro Val Asn	
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Asn Val Lys Lys Val Glu Lys His Gly Pro Gly Arg Trp Val Val Leu	
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 Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
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 Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
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 Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
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 His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
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 Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
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<223> DNA sequence encoding a transmembrane serine
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 Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu
 1 5 10

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 Asn Ser Leu Asp Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu
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 Thr Phe Arg Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu
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 Ala Ser Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys
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 Tyr Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
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 Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr Tyr Phe Leu Cys
 50 55 60
 Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln Leu Cys Asp Gly Glu
 65 70 75 80
 Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu His Cys Val Lys Ser Phe
 85 90 95
 Pro Glu Gly Pro Ala Val Ala Val Arg Leu Ser Lys Asp Arg Ser Thr
 100 105 110
 Leu Gln Val Leu Asp Ser Ala Thr Gly Asn Trp Phe Ser Ala Cys Phe
 115 120 125
 Asp Asn Phe Thr Glu Ala Leu Ala Glu Thr Ala Cys Arg Gln Met Gly

130 135 140
 Tyr Ser Ser Lys Pro Thr Phe Arg Ala Val Glu Ile Gly Pro Asp Gln
 145 150 155 160
 Asp Leu Asp Val Val Glu Ile Thr Glu Asn Ser Gln Glu Leu Arg Met
 165 170 175
 Arg Asn Ser Ser Gly Pro Cys Leu Ser Gly Ser Leu Val Ser Leu His
 180 185 190
 Cys Leu Ala Cys Gly Lys Ser Leu Lys Thr Pro Arg Val Val Gly Gly
 195 200 205
 Glu Glu Ala Ser Val Asp Ser Trp Pro Trp Gln Val Ser Ile Gln Tyr
 210 215 220
 Asp Ile Gln His Val Cys Gly Gly Ser Ile Leu Asp Pro His Trp Val
 225 230 235 240
 Leu Thr Ala Ala His Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp
 245 250 255
 Lys Val Arg Ala Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala
 260 265 270
 Val Ala Lys Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp
 275 280 285
 Asn Asp Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly
 290 295 300
 Thr Val Arg Leu Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro
 305 310 315 320
 Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn Gly
 325 330 335
 Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val Ile Asp
 340 345 350
 Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu Val Thr Glu
 355 360 365
 Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val Asp Thr Cys Gln
 370 375 380
 Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser Asp Gln Trp His Val
 385 390 395 400
 Val Gly Ile Val Ser Trp Gly Tyr Gly Cys Gly Gly Pro Ser Thr Pro
 405 410 415
 Gly Val Tyr Thr Lys Val Ser Ala Tyr Leu Asn Trp Ile Tyr Asn Val
 420 425 430
 Trp Lys Ala Glu Leu
 435

<210> 5
 <211> 708
 <212> DNA
 <213> Homo Sapien

<220>
 <221> CDS
 <222> (1)...(708)
 <223> MTSP4 protease domain cDNA

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 agc ctc cag gtt cgg ggt cga cac atc tgt ggg ggg gcc ctc atc gct 96
 Ser Leu Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala
 20 25 30
 gac cgc tgg gtg ata aca gct gcc cac tgc ttc cag gag gac agc atg 144
 Asp Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met
 35 40 45

gcc tcc acg gtg ctg tgg acc gtg ttc ctg ggc aag gtg tgg cag aac 192
 Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln Asn
 50 55 60

tcg cgc tgg cct gga gag gtg tcc ttc aag gtg agc cgc ctg ctc ctg 240
 Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu Leu Leu
 65 70 75 80

cac ccg tac cac gaa gag gac agc cat gac tac gac gtg gcg ctg ctg 288
 His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val Ala Leu Leu
 85 90 95

cag ctc gac cac ccg gtg gtg cgc tcg gcc gcc gtg cgc ccc gtc tgc 336
 Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val Arg Pro Val Cys
 100 105 110

ctg ccc gcg cgc tcc cac ttc ttc gag ccc ggc ctg cac tgc tgg att 384
 Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly Leu His Cys Trp Ile
 115 120 125

acg ggc tgg ggc gcc ttg cgc gag ggc ggc ccc atc agc aac gct ctg 432
 Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly Pro Ile Ser Asn Ala Leu
 130 135 140

cag aaa gtg gat gtg cag ttg atc cca cag gac ctg tgc agc gag gtc 480
 Gln Lys Val Asp Val Gln Leu Ile Pro Gln Asp Leu Cys Ser Glu Val
 145 150 155 160

tat cgc tac cag gtg acg cca cgc atg ctg tgt gcc gcc tac cgc aag 528
 Tyr Arg Tyr Gln Val Thr Pro Arg Met Leu Cys Ala Gly Tyr Arg Lys
 165 170 175

ggc aag aag gat gcc tgt cag ggt gac tca ggt ggt ccg ctg gtg tgc 576
 Gly Lys Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
 180 185 190

aag gca ctc agt ggc cgc tgg ttc ctg gcg ggc ctg gtc agc tgg ggc 624
 Lys Ala Leu Ser Gly Arg Trp Phe Leu Ala Gly Leu Val Ser Trp Gly
 195 200 205

ctg ggc tgt ggc cgg cct aac tac ttc ggc gtc tac acc cgc atc aca 672
 Leu Gly Cys Gly Arg Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr
 210 215 220

ggt gtg atc agc tgg atc cag caa gtg gtg acc tga 708
 Gly Val Ile Ser Trp Ile Gln Gln Val Val Thr *
 225 230 235

<210> 6
 <211> 235
 <212> PRT
 <213> Homo Sapien

<400> 6
 Ile Val Gly Gly Ala Val Ser Ser Glu Gly Glu Trp Pro Trp Gln Ala
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 Ser Leu Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala
 20 25 30
 Asp Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met
 35 40 45

Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln Asn
 50 55 60
 Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu Leu Leu
 65 70 75 80
 His Pro Tyr His Glu Asp Ser His Asp Tyr Asp Val Ala Leu Leu
 85 90 95
 Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val Arg Pro Val Cys
 100 105 110
 Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly Leu His Cys Trp Ile
 115 120 125
 Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly Pro Ile Ser Asn Ala Leu
 130 135 140
 Gln Lys Val Asp Val Gln Leu Ile Pro Gln Asp Leu Cys Ser Glu Val
 145 150 155 160
 Tyr Arg Tyr Gln Val Thr Pro Arg Met Leu Cys Ala Gly Tyr Arg Lys
 165 170 175
 Gly Lys Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
 180 185 190
 Lys Ala Leu Ser Gly Arg Trp Phe Leu Ala Gly Leu Val Ser Trp Gly
 195 200 205
 Leu Gly Cys Gly Arg Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr
 210 215 220
 Gly Val Ile Ser Trp Ile Gln Gln Val Val Thr
 225 230 235

<210> 7

<211> 3104

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (33)...(2441)

<223> cDNA encoding :MTSP4-L (long form) splice variant

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	1 5	
cag gtg gct ggc ggg cag ggg gac gga ggt gat ggc gag gaa gcg gag		101
Gln Val Ala Gly Gly Gln Gly Asp Gly Gly Asp Gly Glu Glu Ala Glu		
	10 15 20	
ccg gag ggg atg ttc aag gcc tgt gag gac tcc aag aga aaa gcc cgg		149
Pro Glu Gly Met Phe Lys Ala Cys Glu Asp Ser Lys Arg Lys Ala Arg		
	25 30 35	
ggc tac ctc cgc ctg gtg ccc ctg ttt gtg ctg ctg gcc ctg ctc gtg		197
Gly Tyr Leu Arg Leu Val Pro Leu Phe Val Leu Leu Ala Leu Leu Val		
	40 45 50 55	
ctg gct tcg gcg ggg gtg cta ctc tgg tat ttc cta ggg tac aag gcg		245
Leu Ala Ser Ala Gly Val Leu Leu Trp Tyr Phe Leu Gly Tyr Lys Ala		
	60 65 70	
gag gtg atg gtc agc cag gtg tac tca ggc agt ctg cgt gta ctc aat		293
Glu Val Met Val Ser Gln Val Tyr Ser Gly Ser Leu Arg Val Leu Asn		
	75 80 85	
cgc cac ttc tcc cag gat ctt acc cgc cgg gaa tct agt gcc ttc cgc		341
Arg His Phe Ser Gln Asp Leu Thr Arg Arg Glu Ser Ser Ala Phe Arg		

	90		95		100		
	agt gaa acc gcc aaa gcc cag aag atg ctc aag gag ctc atc acc agc					389	
	Ser Glu Thr Ala Lys Ala Gln Lys Met Leu Lys Glu Leu Ile Thr Ser						
	105		110		115		
	acc cgc ctg gga act tac tac aac tcc agc tcc gtc tat tcc ttt ggg					437	
	Thr Arg Leu Gly Thr Tyr Tyr Asn Ser Ser Ser Val Tyr Ser Phe Gly						
	120		125		130		135
	gag gga ccc ctc acc tgc ttc ttc tgg ttc att ctc caa atc ccc gag					485	
	Glu Gly Pro Leu Thr Cys Phe Phe Trp Phe Ile Leu Gln Ile Pro Glu						
		140		145		150	
	cac cgc cgg ctg atg ctg agc ccc gag gtg gtg cag gca ctg ctg gtg					533	
	His Arg Arg Leu Met Leu Ser Pro Glu Val Val Gln Ala Leu Leu Val						
		155		160		165	
	gag gag ctg ctg tcc aca gtc aac agc tcg gct gcc gtc ccc tac agg					581	
	Glu Glu Leu Leu Ser Thr Val Asn Ser Ser Ala Ala Val Pro Tyr Arg						
		170		175		180	
	gcc gag tac gaa gtg gac ccc gag ggc cta gtg atc ctg gaa gcc agt					629	
	Ala Glu Tyr Glu Val Asp Pro Glu Gly Leu Val Ile Leu Glu Ala Ser						
		185		190		195	
	gtg aaa gac ata gct gca ttg aat tcc acg ctg ggt tgt tac cgc tac					677	
	Val Lys Asp Ile Ala Ala Leu Asn Ser Thr Leu Gly Cys Tyr Arg Tyr						
		200		205		210	215
	agc tac gtg ggc cag ggc cag gtc ctc cgg ctg aag ggg cct gac cac					725	
	Ser Tyr Val Gly Gln Gly Gln Val Leu Arg Leu Lys Gly Pro Asp His						
		220		225		230	
	ctg gcc tcc agc tgc ctg tgg cac ctg cag ggc ccc aag gac ctc atg					773	
	Leu Ala Ser Ser Cys Leu Trp His Leu Gln Gly Pro Lys Asp Leu Met						
		235		240		245	
	ctc aaa ctc cgg ctg gag tgg acg ctg gca gag tgc cgg gac cga ctg					821	
	Leu Lys Leu Arg Leu Glu Trp Thr Leu Ala Glu Cys Arg Asp Arg Leu						
		250		255		260	
	gcc atg tat gac gtg gcc ggg ccc ctg gag aag agg ctc atc acc tcg					869	
	Ala Met Tyr Asp Val Ala Gly Pro Leu Glu Lys Arg Leu Ile Thr Ser						
		265		270		275	
	gtg tac ggc tgc agc cgc cag gag ccc gtg gtg gag gtt ctg gcg tcg					917	
	Val Tyr Gly Cys Ser Arg Gln Glu Pro Val Val Glu Val Leu Ala Ser						
		280		285		290	295
	ggg gcc atc atg gcg gtc gtc tgg aag aag ggc ctg cac agc tac tac					965	
	Gly Ala Ile Met Ala Val Val Trp Lys Lys Gly Leu His Ser Tyr Tyr						
		300		305		310	
	gac ccc ttc gtg ctc tcc gtg cag ccg gtg gtc ttc cag gcc tgt gaa					1013	
	Asp Pro Phe Val Leu Ser Val Gln Pro Val Val Phe Gln Ala Cys Glu						
		315		320		325	
	gtg aac ctg acg ctg gac aac agg ctc gac tcc cag ggc gtc ctc agc					1061	
	Val Asn Leu Thr Leu Asp Asn Arg Leu Asp Ser Gln Gly Val Leu Ser						
		330		335		340	

acc	ccg	tac	ttc	ccc	agc	tac	tac	tcg	ccc	caa	acc	cac	tgc	tcc	tgg	1109
Thr	Pro	Tyr	Phe	Pro	Ser	Tyr	Tyr	Ser	Pro	Gln	Thr	His	Cys	Ser	Trp	
	345					350					355					
cac	ctc	acg	gtg	ccc	tct	ctg	gac	tac	ggc	ttg	gcc	ctc	tgg	ttt	gat	1157
His	Leu	Thr	Val	Pro	Ser	Leu	Asp	Tyr	Gly	Leu	Ala	Leu	Trp	Phe	Asp	
360					365					370					375	
gcc	tat	gca	ctg	agg	agg	cag	aag	tat	gat	ttg	ccg	tgc	acc	cag	ggc	1205
Ala	Tyr	Ala	Leu	Arg	Arg	Gln	Lys	Tyr	Asp	Leu	Pro	Cys	Thr	Gln	Gly	
				380					385					390		
cag	tgg	acg	atc	cag	aac	agg	agg	ctg	tgt	ggc	ttg	cgc	atc	ctg	cag	1253
Gln	Trp	Thr	Ile	Gln	Asn	Arg	Arg	Leu	Cys	Gly	Leu	Arg	Ile	Leu	Gln	
			395					400					405			
ccc	tac	gcc	gag	agg	atc	ccc	gtg	gtg	gcc	acg	gcc	ggg	atc	acc	atc	1301
Pro	Tyr	Ala	Glu	Arg	Ile	Pro	Val	Val	Ala	Thr	Ala	Gly	Ile	Thr	Ile	
		410					415					420				
aac	ttc	acc	tcc	cag	atc	tcc	ctc	acc	ggg	ccc	ggg	gtg	cgg	gtg	cac	1349
Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr	Gly	Pro	Gly	Val	Arg	Val	His	
	425					430					435					
tat	ggc	ttg	tac	aac	cag	tcg	gac	ccc	tgc	cct	gga	gag	ttc	ctc	tgt	1397
Tyr	Gly	Leu	Tyr	Asn	Gln	Ser	Asp	Pro	Cys	Pro	Gly	Glu	Phe	Leu	Cys	
440				445					450						455	
tct	gtg	aat	gga	ctc	tgt	gtc	cct	gcc	tgt	gat	ggg	gtc	aag	gac	tgc	1445
Ser	Val	Asn	Gly	Leu	Cys	Val	Pro	Ala	Cys	Asp	Gly	Val	Lys	Asp	Cys	
				460					465					470		
ccc	aac	ggc	ctg	gat	gag	aga	aac	tgc	gtt	tgc	aga	gcc	aca	ttc	cag	1493
Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys	Val	Cys	Arg	Ala	Thr	Phe	Gln	
			475					480					485			
tgc	aaa	gag	gac	agc	aca	tgc	atc	tca	ctg	ccc	aag	gtc	tgt	gat	ggg	1541
Cys	Lys	Glu	Asp	Ser	Thr	Cys	Ile	Ser	Leu	Pro	Lys	Val	Cys	Asp	Gly	
		490					495					500				
cag	cct	gat	tgt	ctc	aac	ggc	agc	gac	gaa	gag	cag	tgc	cag	gaa	ggg	1589
Gln	Pro	Asp	Cys	Leu	Asn	Gly	Ser	Asp	Glu	Glu	Gln	Cys	Gln	Glu	Gly	
	505					510					515					
gtg	cca	tgt	ggg	aca	ttc	acc	ttc	cag	tgt	gag	gac	cgg	agc	tgc	gtg	1637
Val	Pro	Cys	Gly	Thr	Phe	Thr	Phe	Gln	Cys	Glu	Asp	Arg	Ser	Cys	Val	
520					525					530					535	
aag	aag	ccc	aac	ccg	cag	tgt	gat	ggg	cgg	ccc	gac	tgc	agg	gac	ggc	1685
Lys	Lys	Pro	Asn	Pro	Gln	Cys	Asp	Gly	Arg	Pro	Asp	Cys	Arg	Asp	Gly	
				540					545					550		
tcg	gat	gag	gag	cac	tgt	gaa	tgt	ggc	ctc	cag	ggc	ccc	tcc	agc	cgc	1733
Ser	Asp	Glu	Glu	His	Cys	Glu	Cys	Gly	Leu	Gln	Gly	Pro	Ser	Ser	Arg	
			555					560					565			
att	gtt	ggt	gga	gct	gtg	tcc	tcc	gag	ggt	gag	tgg	cca	tgg	cag	gcc	1781
Ile	Val	Gly	Gly	Ala	Val	Ser	Ser	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	
		570					575					580				
agc	ctc	cag	ggt	cgg	ggt	cga	cac	atc	tgt	ggg	ggg	gcc	ctc	atc	gct	1829
Ser	Leu	Gln	Val	Arg	Gly	Arg	His	Ile	Cys	Gly	Gly	Ala	Leu	Ile	Ala	

585	590	595	
gac cgc tgg gtg ata aca gct gcc cac tgc ttc cag gag gac agc atg Asp Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met 600 605 610 615			1877
gcc tcc acg gtg ctg tgg acc gtg ttc ctg ggc aag gtg tgg cag aac Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln Asn 620 625 630			1925
tcg cgc tgg cct gga gag gtg tcc ttc aag gtg agc cgc ctg ctc ctg Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu Leu Leu 635 640 645			1973
cac ccg tac cac gaa gag gac agc cat gac tac gac gtg gcg ctg ctg His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val Ala Leu Leu 650 655 660			2021
cag ctc gac cac ccg gtg gtg cgc tcg gcc gcc gtg cgc ccc gtc tgc Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val Arg Pro Val Cys 665 670 675			2069
ctg ccc gcg cgc tcc cac ttc ttc gag ccc ggc ctg cac tgc tgg att Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly Leu His Cys Trp Ile 680 685 690 695			2117
acg ggc tgg ggc gcc ttg cgc gag ggc ggc ccc atc agc aac gct ctg Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly Pro Ile Ser Asn Ala Leu 700 705 710			2165
cag aaa gtg gat gtg cag ttg atc cca cag gac ctg tgc agc gag gtc Gln Lys Val Asp Val Gln Leu Ile Pro Gln Asp Leu Cys Ser Glu Val 715 720 725			2213
tat cgc tac cag gtg acg cca cgc atg ctg tgt gcc ggc tac cgc aag Tyr Arg Tyr Gln Val Thr Pro Arg Met Leu Cys Ala Gly Tyr Arg Lys 730 735 740			2261
ggc aag aag gat gcc tgt cag ggt gac tca ggt ggt ccg ctg gtg tgc Gly Lys Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys 745 750 755			2309
aag gca ctc agt ggc cgc tgg ttc ctg gcg ggg ctg gtc agc tgg ggc Lys Ala Leu Ser Gly Arg Trp Phe Leu Ala Gly Leu Val Ser Trp Gly 760 765 770 775			2357
ctg ggc tgt ggc cgg cct aac tac ttc ggc gtc tac acc cgc atc aca Leu Gly Cys Gly Arg Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr 780 785 790			2405
ggt gtg atc agc tgg atc cag caa gtg gtg acc tga ggaactgccc Gly Val Ile Ser Trp Ile Gln Gln Val Val Thr * 795 800			2451
cctgcaaaag cagggccac ctctggact cagagagccc agggcaactg ccaagcaggg ggacaagtat tctggcgggg ggtgggggag agagcaggcc ctgtggtggc aggaggggca tctgttttcg tccctgatgt ctgtccagta tggcaggagg atgagaagtg ccagcagttg ggggtcaaga cgtcccttga ggaccacaggc ccacaccccag cccttttgcc tcccaattct ctctcctcgc tccccttcc cactgctgc ctaatgcaag gcagtggctc agcagcaaga atgctggttc tacatcccga ggagtgtctg aggtgcgccc cactctgtac agaggctgtt tgggcagcct tgcctccaga gagcagattc cagcttcgga agcccctggt ctaactggg atctgggaat ggaaggtgct cccatcgagg gggaccctca gaggcctgga gactgccagg			2511 2571 2631 2691 2751 2811 2871 2931

tgggcctgct gccactgtaa gccaaaaggt ggggaagtcc tgactccagg gtccttgccc 2991
 caccctgcc tgccacctgg gccctcacag cccagacct cactgggagg tgagctcagc 3051
 tgccttttgg aataaagctg cctgatgcaa aaaaaaaaaa aaaaaaaaaa aaa 3104

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 <211> 802
 <212> PRT
 <213> Homo Sapien

<400> 8
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 Gly Asp Gly Glu Glu Ala Glu Pro Glu Gly Met Phe Lys Ala Cys Glu
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 Asp Ser Lys Arg Lys Ala Arg Gly Tyr Leu Arg Leu Val Pro Leu Phe
 35 40 45
 Val Leu Leu Ala Leu Leu Val Leu Ala Ser Ala Gly Val Leu Leu Trp
 50 55 60
 Tyr Phe Leu Gly Tyr Lys Ala Glu Val Met Val Ser Gln Val Tyr Ser
 65 70 75 80
 Gly Ser Leu Arg Val Leu Asn Arg His Phe Ser Gln Asp Leu Thr Arg
 85 90 95
 Arg Glu Ser Ser Ala Phe Arg Ser Glu Thr Ala Lys Ala Gln Lys Met
 100 105 110
 Leu Lys Glu Leu Ile Thr Ser Thr Arg Leu Gly Thr Tyr Tyr Asn Ser
 115 120 125
 Ser Ser Val Tyr Ser Phe Gly Glu Gly Pro Leu Thr Cys Phe Phe Trp
 130 135 140
 Phe Ile Leu Gln Ile Pro Glu His Arg Arg Leu Met Leu Ser Pro Glu
 145 150 155 160
 Val Val Gln Ala Leu Leu Val Glu Glu Leu Leu Ser Thr Val Asn Ser
 165 170 175
 Ser Ala Ala Val Pro Tyr Arg Ala Glu Tyr Glu Val Asp Pro Glu Gly
 180 185 190
 Leu Val Ile Leu Glu Ala Ser Val Lys Asp Ile Ala Ala Leu Asn Ser
 195 200 205
 Thr Leu Gly Cys Tyr Arg Tyr Ser Tyr Val Gly Gln Gly Gln Val Leu
 210 215 220
 Arg Leu Lys Gly Pro Asp His Leu Ala Ser Ser Cys Leu Trp His Leu
 225 230 235 240
 Gln Gly Pro Lys Asp Leu Met Leu Lys Leu Arg Leu Glu Trp Thr Leu
 245 250 255
 Ala Glu Cys Arg Asp Arg Leu Ala Met Tyr Asp Val Ala Gly Pro Leu
 260 265 270
 Glu Lys Arg Leu Ile Thr Ser Val Tyr Gly Cys Ser Arg Gln Glu Pro
 275 280 285
 Val Val Glu Val Leu Ala Ser Gly Ala Ile Met Ala Val Val Trp Lys
 290 295 300
 Lys Gly Leu His Ser Tyr Tyr Asp Pro Phe Val Leu Ser Val Gln Pro
 305 310 315 320
 Val Val Phe Gln Ala Cys Glu Val Asn Leu Thr Leu Asp Asn Arg Leu
 325 330 335
 Asp Ser Gln Gly Val Leu Ser Thr Pro Tyr Phe Pro Ser Tyr Tyr Ser
 340 345 350
 Pro Gln Thr His Cys Ser Trp His Leu Thr Val Pro Ser Leu Asp Tyr
 355 360 365
 Gly Leu Ala Leu Trp Phe Asp Ala Tyr Ala Leu Arg Arg Gln Lys Tyr
 370 375 380
 Asp Leu Pro Cys Thr Gln Gly Gln Trp Thr Ile Gln Asn Arg Arg Leu
 385 390 395 400
 Cys Gly Leu Arg Ile Leu Gln Pro Tyr Ala Glu Arg Ile Pro Val Val
 405 410 415

Ala Thr Ala Gly Ile Thr Ile Asn Phe Thr Ser Gln Ile Ser Leu Thr
 420 425 430
 Gly Pro Gly Val Arg Val His Tyr Gly Leu Tyr Asn Gln Ser Asp Pro
 435 440 445
 Cys Pro Gly Glu Phe Leu Cys Ser Val Asn Gly Leu Cys Val Pro Ala
 450 455 460
 Cys Asp Gly Val Lys Asp Cys Pro Asn Gly Leu Asp Glu Arg Asn Cys
 465 470 475 480
 Val Cys Arg Ala Thr Phe Gln Cys Lys Glu Asp Ser Thr Cys Ile Ser
 485 490 495
 Leu Pro Lys Val Cys Asp Gly Gln Pro Asp Cys Leu Asn Gly Ser Asp
 500 505 510
 Glu Glu Gln Cys Gln Glu Gly Val Pro Cys Gly Thr Phe Thr Phe Gln
 515 520 525
 Cys Glu Asp Arg Ser Cys Val Lys Lys Pro Asn Pro Gln Cys Asp Gly
 530 535 540
 Arg Pro Asp Cys Arg Asp Gly Ser Asp Glu Glu His Cys Glu Cys Gly
 545 550 555 560
 Leu Gln Gly Pro Ser Ser Arg Ile Val Gly Gly Ala Val Ser Ser Glu
 565 570 575
 Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln Val Arg Gly Arg His Ile
 580 585 590
 Cys Gly Gly Ala Leu Ile Ala Asp Arg Trp Val Ile Thr Ala Ala His
 595 600 605
 Cys Phe Gln Glu Asp Ser Met Ala Ser Thr Val Leu Trp Thr Val Phe
 610 615 620
 Leu Gly Lys Val Trp Gln Asn Ser Arg Trp Pro Gly Glu Val Ser Phe
 625 630 635 640
 Lys Val Ser Arg Leu Leu His Pro Tyr His Glu Glu Asp Ser His
 645 650 655
 Asp Tyr Asp Val Ala Leu Leu Gln Leu Asp His Pro Val Val Arg Ser
 660 665 670
 Ala Ala Val Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu
 675 680 685
 Pro Gly Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly
 690 695 700
 Gly Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro
 705 710 715 720
 Gln Asp Leu Cys Ser Glu Val Tyr Arg Tyr Gln Val Thr Pro Arg Met
 725 730 735
 Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln Gly Asp
 740 745 750
 Ser Gly Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg Trp Phe Leu
 755 760 765
 Ala Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg Pro Asn Tyr Phe
 770 775 780
 Gly Val Tyr Thr Arg Ile Thr Gly Val Ile Ser Trp Ile Gln Gln Val
 785 790 795 800
 Val Thr

<210> 9

<211> 2672

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (33)...(2009)

<223> cDNA encoding: MTSP4-S (short form) splice variant

<400> 9

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Gln	Trp	Thr	Ile	Gln	Asn	Arg	Arg	Leu	Cys	Gly	Leu	Arg	Ile	Leu	Gln					
		250					255					260								
ccc	tac	gcc	gag	agg	atc	ccc	gtg	gtg	gcc	acg	gcc	ggg	atc	acc	atc	869				
Pro	Tyr	Ala	Glu	Arg	Ile	Pro	Val	Val	Ala	Thr	Ala	Gly	Ile	Thr	Ile					
	265					270					275									
aac	ttc	acc	tcc	cag	atc	tcc	ctc	acc	ggg	ccc	ggg	gtg	cgg	gtg	cac	917				
Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr	Gly	Pro	Gly	Val	Arg	Val	His					
280					285					290					295					
tat	ggc	ttg	tac	aac	cag	tcg	gac	ccc	tgc	cct	gga	gag	ttc	ctc	tgt	965				
Tyr	Gly	Leu	Tyr	Asn	Gln	Ser	Asp	Pro	Cys	Pro	Gly	Glu	Phe	Leu	Cys					
				300					305					310						
tct	gtg	aat	gga	ctc	tgt	gtc	cct	gcc	tgt	gat	ggg	gtc	aag	gac	tgc	1013				
Ser	Val	Asn	Gly	Leu	Cys	Val	Pro	Ala	Cys	Asp	Gly	Val	Lys	Asp	Cys					
			315					320					325							
ccc	aac	ggc	ctg	gat	gag	aga	aac	tgc	gtt	tgc	aga	gcc	aca	ttc	cag	1061				
Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys	Val	Cys	Arg	Ala	Thr	Phe	Gln					
		330					335					340								
tgc	aaa	gag	gac	agc	aca	tgc	atc	tca	ctg	ccc	aag	gtc	tgt	gat	ggg	1109				
Cys	Lys	Glu	Asp	Ser	Thr	Cys	Ile	Ser	Leu	Pro	Lys	Val	Cys	Asp	Gly					
	345					350					355									
cag	cct	gat	tgt	ctc	aac	ggc	agc	gac	gaa	gag	cag	tgc	cag	gaa	ggg	1157				
Gln	Pro	Asp	Cys	Leu	Asn	Gly	Ser	Asp	Glu	Glu	Gln	Cys	Gln	Glu	Gly					
360					365					370					375					
gtg	cca	tgt	ggg	aca	ttc	acc	ttc	cag	tgt	gag	gac	cgg	agc	tgc	gtg	1205				
Val	Pro	Cys	Gly	Thr	Phe	Thr	Phe	Gln	Cys	Glu	Asp	Arg	Ser	Cys	Val					
				380				385						390						
aag	aag	ccc	aac	ccg	cag	tgt	gat	ggg	cgg	ccc	gac	tgc	agg	gac	ggc	1253				
Lys	Lys	Pro	Asn	Pro	Gln	Cys	Asp	Gly	Arg	Pro	Asp	Cys	Arg	Asp	Gly					
			395					400					405							
tcg	gat	gag	gag	cac	tgt	gaa	tgt	ggc	ctc	cag	ggc	ccc	tcc	agc	cgc	1301				
Ser	Asp	Glu	Glu	His	Cys	Glu	Cys	Gly	Leu	Gln	Gly	Pro	Ser	Ser	Arg					
		410				415						420								
att	gtt	ggg	gga	gct	gtg	tcc	tcc	gag	ggg	gag	tgg	cca	tgg	cag	gcc	1349				
Ile	Val	Gly	Gly	Ala	Val	Ser	Ser	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala					
	425					430					435									
agc	ctc	cag	gtt	cgg	ggg	cga	cac	atc	tgt	ggg	ggg	gcc	ctc	atc	gct	1397				
Ser	Leu	Gln	Val	Arg	Gly	Arg	His	Ile	Cys	Gly	Gly	Ala	Leu	Ile	Ala					
440					445					450					455					
gac	cgc	tgg	gtg	ata	aca	gct	gcc	cac	tgc	ttc	cag	gag	gac	agc	atg	1445				
Asp	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	Cys	Phe	Gln	Glu	Asp	Ser	Met					
				460					465					470						
gcc	tcc	acg	gtg	ctg	tgg	acc	gtg	ttc	ctg	ggc	aag	gtg	tgg	cag	aac	1493				
Ala	Ser	Thr	Val	Leu	Trp	Thr	Val	Phe	Leu	Gly	Lys	Val		Gln	Asn					
			475					480					485							

tcg cgc tgg cct gga gag gtg tcc ttc aag gtg agc cgc ctg ctc ctg 1541
 Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu Leu Leu
 490 495 500

cac ccg tac cac gaa gag gac agc cat gac tac gac gtg gcg ctg ctg 1589
 His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val Ala Leu Leu
 505 510 515

cag ctc gac cac ccg gtg gtg cgc tgc gcc gcc gtg cgc ccc gtc tgc 1637
 Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val Arg Pro Val Cys
 520 525 530 535

ctg ccc gcg cgc tcc cac ttc ttc gag ccc gcc ctg cac tgc tgg att 1685
 Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly Leu His Cys Ile
 540 545 550

acg ggc tgg ggc gcc ttg cgc gag ggc gcc ccc atc agc aac gct ctg 1733
 Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly Pro Ile Ser Asn Ala Leu
 555 560 565

cag aaa gtg gat gtg cag ttg atc cca cag gac ctg tgc agc gag gtc 1781
 Gln Lys Val Asp Val Gln Leu Ile Pro Gln Asp Leu Cys Ser Glu Val
 570 575 580

tat cgc tac cag gtg acg cca cgc atg ctg tgt gcc gcc tac cgc aag 1829
 Tyr Arg Tyr Gln Val Thr Pro Arg Met Leu Cys Ala Gly Tyr Arg Lys
 585 590 595

ggc aag aag gat gcc tgt cag ggt gac tca ggt ggt ccg ctg gtg tgc 1877
 Gly Lys Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
 600 605 610 615

aag gca ctc agt ggc cgc tgg ttc ctg gcg ggg ctg gtc agc tgg ggc 1925
 Lys Ala Leu Ser Gly Arg Trp Phe Leu Ala Gly Leu Val Ser Trp Gly
 620 625 630

ctg ggc tgt ggc cgg cct aac tac ttc gcc gtc tac acc cgc atc aca 1973
 Leu Gly Cys Gly Arg Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr
 635 640 645

ggt gtg atc agc tgg atc cag caa gtg gtg acc tga ggaactgccc 2019
 Gly Val Ile Ser Trp Ile Gln Gln Val Val Thr *
 650 655

ccctgcaaag cagggccac ctctgggact cagagagccc agggcaactg ccaagcaggg 2079
 ggacaagtat tctggcgagg ggtgggggag agagcaggcc ctgtggtggc aggaggggca 2139
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 ggggtcaaga cgtcccttga ggacccaggc ccacacccag cccttttgcc tcccaattct 2259
 ctctcctccg tccccttccct cactgtctgc ctaatgcaag gcagtggctc agcagcaaga 2319
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 tgggcctgct gccactgtaa gccaaaaggt ggggaagtcc tgactccagg gtccttgccc 2559
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<210> 10
 <211> 658
 <212> PRT
 <213> Homo Sapien
 <400> 10

Met Pro Val Ala Glu Ala Pro Gln Val Ala Gly Gly Gln Gly Asp Gly
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 Gly Asp Gly Glu Glu Ala Glu Pro Glu Gly Met Phe Lys Ala Cys Glu
 20 25 30
 Asp Ser Lys Arg Lys Ala Arg Gly Tyr Leu Arg Leu Val Pro Leu Phe
 35 40 45
 Val Leu Leu Ala Leu Leu Val Leu Ala Ser Ala Gly Val Leu Leu Trp
 50 55 60
 Tyr Phe Leu Gly Tyr Lys Ala Glu Val Met Val Ser Gln Val Tyr Ser
 65 70 75 80
 Gly Ser Leu Arg Val Leu Asn Arg His Phe Ser Gln Asp Leu Thr Arg
 85 90 95
 Arg Glu Ser Ser Ala Phe Arg Ser Glu Thr Ala Lys Ala Gln Lys Met
 100 105 110
 Leu Lys Glu Leu Ile Thr Ser Thr Arg Leu Gly Thr Tyr Tyr Asn Ser
 115 120 125
 Ser Ser Val Tyr Ser Phe Gly Val Tyr Gly Cys Ser Arg Gln Glu Pro
 130 135 140
 Val Val Glu Val Leu Ala Ser Gly Ala Ile Met Ala Val Val Trp Lys
 145 150 155 160
 Lys Gly Leu His Ser Tyr Tyr Asp Pro Phe Val Leu Ser Val Gln Pro
 165 170 175
 Val Val Phe Gln Ala Cys Glu Val Asn Leu Thr Leu Asp Asn Arg Leu
 180 185 190
 Asp Ser Gln Gly Val Leu Ser Thr Pro Tyr Phe Pro Ser Tyr Tyr Ser
 195 200 205
 Pro Gln Thr His Cys Ser Trp His Leu Thr Val Pro Ser Leu Asp Tyr
 210 215 220
 Gly Leu Ala Leu Trp Phe Asp Ala Tyr Ala Leu Arg Arg Gln Lys Tyr
 225 230 235 240
 Asp Leu Pro Cys Thr Gln Gly Gln Trp Thr Ile Gln Asn Arg Arg Leu
 245 250 255
 Cys Gly Leu Arg Ile Leu Gln Pro Tyr Ala Glu Arg Ile Pro Val Val
 260 265 270
 Ala Thr Ala Gly Ile Thr Ile Asn Phe Thr Ser Gln Ile Ser Leu Thr
 275 280 285
 Gly Pro Gly Val Arg Val His Tyr Gly Leu Tyr Asn Gln Ser Asp Pro
 290 295 300
 Cys Pro Gly Glu Phe Leu Cys Ser Val Asn Gly Leu Cys Val Pro Ala
 305 310 315 320
 Cys Asp Gly Val Lys Asp Cys Pro Asn Gly Leu Asp Glu Arg Asn Cys
 325 330 335
 Val Cys Arg Ala Thr Phe Gln Cys Lys Glu Asp Ser Thr Cys Ile Ser
 340 345 350
 Leu Pro Lys Val Cys Asp Gly Gln Pro Asp Cys Leu Asn Gly Ser Asp
 355 360 365
 Glu Glu Gln Cys Gln Glu Gly Val Pro Cys Gly Thr Phe Thr Phe Gln
 370 375 380
 Cys Glu Asp Arg Ser Cys Val Lys Lys Pro Asn Pro Gln Cys Asp Gly
 385 390 395 400
 Arg Pro Asp Cys Arg Asp Gly Ser Asp Glu Glu His Cys Glu Cys Gly
 405 410 415
 Leu Gln Gly Pro Ser Ser Arg Ile Val Gly Gly Ala Val Ser Ser Glu
 420 425 430
 Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln Val Arg Gly Arg His Ile
 435 440 445
 Cys Gly Gly Ala Leu Ile Ala Asp Arg Trp Val Ile Thr Ala Ala His
 450 455 460
 Cys Phe Gln Glu Asp Ser Met Ala Ser Thr Val Leu Trp Thr Val Phe
 465 470 475 480
 Leu Gly Lys Val Trp Gln Asn Ser Arg Trp Pro Gly Glu Val Ser Phe
 485 490 495

Lys Val Ser Arg Leu Leu Leu His Pro Tyr His Glu Glu Asp Ser His
 500 505 510
 Asp Tyr Asp Val Ala Leu Leu Gln Leu Asp His Pro Val Val Arg Ser
 515 520 525
 Ala Ala Val Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu
 530 535 540
 Pro Gly Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly
 545 550 555
 Gly Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro
 565 570 575
 Gln Asp Leu Cys Ser Glu Val Tyr Arg Tyr Gln Val Thr Pro Arg Met
 580 585 590
 Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln Gly Asp
 595 600 605
 Ser Gly Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg Trp Phe Leu
 610 615 620
 Ala Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg Pro Asn Tyr Phe
 625 630 635
 Gly Val Tyr Thr Arg Ile Thr Gly Val Ile Ser Trp Ile Gln Gln Val
 645 650 655
 Val Thr

<210> 11
 <211> 1656
 <212> DNA
 <213> Homo Sapien

<220>
 <221> CDS
 <222> (268)...(1629)
 <223> DNA sequence encoding a transmembrane serine
 protease (MTSP-6) protein

<400> 11
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 ttgggactcg ggaattatga ctgttttttg ttaatcgata ctgaatgcgc tttgtgtgga 120
 ctgtcgaatt tcaaagattt accgtatgac caagatgcac ctgatgctac aagtataaat 180
 aggggaacaa atgcttttctg ttcttctctg gctaaggagg tagaggtgga ggcggagccg 240
 gatgtcagag gtcctgaaat agtcacc atg ggg gaa aat gat ccg cct gct gtt 294
 Met Gly Glu Asn Asp Pro Pro Ala Val
 1 5

 gaa gcc ccc ttc tca ttc cga tcg ctt ttt ggc ctt gat gat ttg aaa 342
 Glu Ala Pro Phe Ser Phe Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys
 10 15 20 25

 ata agt cct gtt gca cca gat gca gat gct gtt gct gca cag atc ctg 390
 Ile Ser Pro Val Ala Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu
 30 35 40

 tca ctg ctg cca ttg aag ttt ttt cca atc atc gtc att ggg atc att 438
 Ser Leu Leu Pro Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile
 45 50 55

 gca ttg ata tta gca ctg gcc att ggt ctg ggc atc cac ttc gac tgc 486
 Ala Leu Ile Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys
 60 65 70

 tca ggg aag tac aga tgt cgc tca tcc ttt aag tgt atc gag ctg ata 534
 Ser Gly Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile
 75 80 85

gct cga tgt gac gga gtc tgc gat tgc aaa gac ggg gag gac gag tac	582
Ala Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr	
90 95 100 105	
cgc tgt gtc cgg gtg ggt ggt cag aat gcc gtg ctc cag gtg ttc aca	630
Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe Thr	
110 115 120	
gct gct tgc tgg aag acc atg tgc tcc gat gac tgg aag ggt cac tac	678
Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly His Tyr	
125 130 135	
gca aat gtt gcc tgt gcc caa ctg ggt ttc cca agc tat gta agt tca	726
Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr Val Ser Ser	
140 145 150	
gat aac ctc aga gtg agc tgc cta gag ggg cag ttc cgg gag gag ttt	774
Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe Arg Glu Glu Phe	
155 160 165	
gtg tcc atc gat cac ctc ttg cca gat gac aag gtg act gca tta cac	822
Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys Val Thr Ala Leu His	
170 175 180 185	
cac tca gta tat gtg agg gag gga tgt gcc tct ggc cac gtg gtt acc	870
His Ser Val Tyr Val Arg Glu Gly Cys Ala Ser Gly His Val Val Thr	
190 195 200	
ttg cag tgc aca gcc tgt ggt cat aga agg ggc tac agc tca cgc atc	918
Leu Gln Cys Thr Ala Cys Gly His Arg Arg Gly Tyr Ser Ser Arg Ile	
205 210 215	
gtg ggt gga aac atg tcc ttg ctc tgc cag tgg ccc tgg cag gcc agc	966
Val Gly Gly Asn Met Ser Leu Leu Ser Gln Trp Pro Trp Gln Ala Ser	
220 225 230	
ctt cag ttc cag ggc tac cac ctg tgc ggg ggc tct gtc atc acg ccc	1014
Leu Gln Phe Gln Gly Tyr His Leu Cys Gly Gly Ser Val Ile Thr Pro	
235 240 245	
ctg tgg atc atc act gct gca cac tgt gtt tat gac ttg tac ctc ccc	1062
Leu Trp Ile Ile Thr Ala Ala His Cys Val Tyr Asp Leu Tyr Leu Pro	
250 255 260 265	
aag tca tgg acc atc cag gtg ggt cta gtt tcc ctg ttg gac aat cca	1110
Lys Ser Trp Thr Ile Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro	
270 275 280	
gcc cca tcc cac ttg gtg gag aag att gtc tac cac agc aag tac aag	1158
Ala Pro Ser His Leu Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys	
285 290 295	
cca aag agg ctg ggc aat gac atc gcc ctt atg aag ctg gcc ggg cca	1206
Pro Lys Arg Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro	
300 305 310	
ctc acg ttc aat gaa atg atc cag cct gtg tgc ctg ccc aac tct gaa	1254
Leu Thr Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu	
315 320 325	
gag aac ttc ccc gat gga aaa gtg tgc tgg acg tca gga tgg ggg gcc	1302

Glu Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala
 330 335 340 345
 aca gag gat gga ggt gac gcc tcc cct gtc ctg aac cac gcg gcc gtc 1350
 Thr Glu Asp Gly Asp Ala Ser Pro Val Leu Asn His Ala Val 360
 350
 cct ttg att tcc aac aag atc tgc aac cac agg gac gtg tac ggt ggc 1398
 Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr Gly Gly 375
 365 370
 atc atc tcc ccc tcc atg ctc tgc gcg ggc tac ctg acg ggt ggc gtg 1446
 Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr Gly Gly Val 390
 380 385
 gac agc tgc cag ggg gac agc ggg ggg ccc ctg gtg tgt caa gag agg 1494
 Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Glu Arg 405
 395 400
 agg ctg tgg aag tta gtg gga gcg acc agc ttt ggc atc ggc tgc gca 1542
 Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe Gly Ile Gly Cys Ala 425
 410 415 420
 gag gtg aac aag cct ggg gtg tac acc cgt gtc acc tcc ttc ctg gac 1590
 Glu Val Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ser Phe Leu Asp 440
 430 435
 tgg atc cac gag cag atg gag aga gac cta aaa acc tga agaggaaggg 1639
 Trp Ile His Glu Gln Met Glu Arg Asp Leu Lys Thr * 450
 445
 gataagtagc cacctga 1656
 <210> 12
 <211> 453
 <212> PRT
 <213> Homo Sapien
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 20 25 30
 Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro Leu Lys Phe
 35 40 45
 Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile Leu Ala Leu Ala
 50 55 60
 Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly Lys Tyr Arg Cys Arg
 65 70 75 80
 Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala Arg Cys Asp Gly Val Ser
 85 90 95
 Asp Cys Lys Asp Gly Glu Asp Glu Tyr Arg Cys Val Arg Val Gly Gly
 100 105 110
 Gln Asn Ala Val Leu Gln Val Phe Thr Ala Ala Ser Trp Lys Thr Met
 115 120 125
 Cys Ser Asp Asp Trp Lys Gly His Tyr Ala Asn Val Ala Cys Ala Gln
 130 135 140
 Leu Gly Phe Pro Ser Tyr Val Ser Ser Asp Asn Leu Arg Val Ser Ser
 145 150 155 160
 Leu Glu Gly Gln Phe Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu
 165 170 175
 Pro Asp Asp Lys Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu

Gly Cys Ala Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly
 180 195 200 205
 His Arg Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu
 210 215 220
 Leu Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His
 225 230 235 240
 Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala Ala
 245 250 255
 His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile Gln Val
 260 265 270
 Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His Leu Val Glu
 275 280 285
 Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg Leu Gly Asn Asp
 290 295 300
 Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr Phe Asn Glu Met Ile
 305 310 315 320
 Gln Pro Val Cys Leu Pro Asn Ser Glu Glu Asn Phe Pro Asp Gly Lys
 325 330 335
 Val Cys Trp Thr Ser Gly Trp Gly Ala Thr Glu Asp Gly Gly Asp Ala
 340 345 350
 Ser Pro Val Leu Asn His Ala Ala Val Pro Leu Ile Ser Asn Lys Ile
 355 360 365
 Cys Asn His Arg Asp Val Tyr Gly Gly Ile Ile Ser Pro Ser Met Leu
 370 375 380
 Cys Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln Gly Asp Ser
 385 390 395 400
 Gly Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly
 405 410 415
 Ala Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val
 420 425 430
 Tyr Thr Arg Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu
 435 440 445
 Arg Asp Leu Lys Thr
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<210> 13
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide Primer

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 <222> (0)...(0)
 <223> N= Inosine

<400> 13
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23

<210> 14
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
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<221> misc_feature
 <222> (0)...(0)
 <223> N= Inosine

<400> 14
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 <210> 15
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer

 <400> 15
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 <210> 16
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer

 <400> 16
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 <210> 17
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer

 <400> 17
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 <210> 18
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <400> 18
 gcagacgatg cgtaccaggg ggaagtc 27

 <210> 19
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer

 <400> 19
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 <210> 20
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer

<400> 20
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 <210> 21
 <211> 27
 <212> DNA
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 <220>
 <223> Oligonucleotide Primer

 <400> 21
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 <210> 22
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Primer

 <400> 22
 cctcgcgcaa ggcgccccag cccg 24

 <210> 23
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Primer

 <400> 23
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 <210> 24
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Primer

 <400> 24
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 <210> 25
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Primer

 <400> 25
 cctcgcgcaa ggcgccccag cccg 24

 <210> 26
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide Primer

 <400> 26
 tcacgcgcca gaggtgatc agtgag 26

 <210> 27
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Primer

 <400> 27
 cctcctcagt gcataggcat caaaccag 28

 <210> 28
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Primer

 <400> 28
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 <210> 29
 <211> 31
 <212> DNA
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 <220>
 <223> Oligonucleotide Primer

 <400> 29
 aggtgggcct tgctttgcag gggggcagtt c 31

 <210> 30
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Primer

 <400> 30
 tcacgcacgc tgggtggaac atgtcc 26

 <210> 31
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Primer

 <400> 31
 acccacctcc atctgctcgt ggatcc 26

 <210> 32

<211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer

 <400> 32
 ccacagcctc ctctcttgac acaccag 27

 <210> 33
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer

 <400> 33
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 <210> 34
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer

 <400> 34
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 <210> 35
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer

 <400> 35
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 <210> 36
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer

 <400> 36
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 <210> 37
 <211> 27
 <212> DNA
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 gaagagtatg agtattcaac atttccgtgt cgcccttatt cccttttttg cggcattttg 2160
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 agcggaag 3908

<210> 47
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer

<400> 47 46
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<210> 48
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer

<400> 48 32
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<210> 49
 <211> 3147
 <212> DNA
 <213> Homo Sapien

<220>
 <221> CDS
 <222> (1865)...(2590)
 <223> Nucleic acid sequence of protease domain of MTSP1

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 gaaggacttc ggcgcgggac tcaagtacaa ctcccgccac gagaaagtga atggcttgga 180
 ggaaggcgtg gagttcctgc cagtcaacaa cgtaagaag gtggaaaagc atggcccggg 240
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 cttcctgggtg tggcatttgc agtaccggga cgtgcgtgtc cagaaggtct tcaatggcta 360
 catgaggatc acaaattgaga attttgtgga tgcctacgag aactccaact cactgagtt 420
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 cctgggcccc taccacaagg agtcggctgt gacggccttc agcgagggca gcgtcatcgc 540
 ctactactgg tctgagttca gcatcccgca gcacctggtg gaggaggccg agcgcgtcat 600
 ggccgaggag cgcgtagtca tgctgcccc gcgggcgcgc tccctgaagt cctttgtggt 660
 cactcagtg gtggctttcc ccacggactc caaaacagta cagaggaccc aggacaacag 720
 ctgcagcttt ggcctgcacg cccgcggtgt ggagctgatg cgcttcacca cgcccggtt 780
 ccctgacagc ccctaccccg ctcatgcccg ctgccagtgg gccctgcggg gggacgccga 840
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 tagcgacggc tcagatgaga aggactgcga ctgtgggctg cggtcattca cgagacaggc 1860
 tcgt gtt gtt ggg ggc acg gat gcg gat gag ggc gag tgg ccc tgg cag 1909
 Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln
 1 5 10 15

gta agc ctg cat gct ctg ggc cag ggc cac atc tgc ggt gct tcc ctc 1957
 Val Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu
 20 25 30

atc tct ccc aac tgg ctg gtc tct gcc gca cac tgc tac atc gat gac 2005
 Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp
 35 40 45

aga gga ttc agg tac tca gac ccc acg cag tgg acg gcc ttc ctg ggc 2053
 Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly
 50 55 60

ttg cac gac cag agc cag cgc agc gcc cct ggg gtg cag gag cgc agg 2101
 Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg
 65 70 75

ctc aag cgc atc atc tcc cac ccc ttc ttc aat gac ttc acc ttc gac 2149
 Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp
 80 85 90 95

tat gac atc gcg ctg ctg gag ctg gag aaa ccg gca gag tac agc tcc 2197
 Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser
 100 105 110

atg gtg cgg ccc atc tgc ctg ccg gac gcc tcc cat gtc ttc cct gcc 2245
 Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala
 115 120 125

ggc aag gcc atc tgg gtc acg ggc tgg gga cac acc cag tat gga ggc 2293
 Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly
 130 135 140

act ggc gcg ctg atc ctg caa aag ggt gag atc cgc gtc atc aac cag 2341
 Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln
 145 150 155

acc acc tgc gag aac ctc ctg ccg cag cag atc acg ccg cgc atg atg 2389
 Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met
 160 165 170 175

tgc gtg ggc ttc ctc agc ggc ggc gtg gac tcc tgc cag ggt gat tcc 2437
 Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser
 180 185 190

ggg gga ccc ctg tcc agc gtg gag gcg gat ggg cgg atc ttc cag gcc 2485
 Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala
 195 200 205

ggt gtg gtg agc tgg gga gac ggc tgc gct cag agg aac aag cca ggc 2533
 Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly
 210 215 220

gtg tac aca agg ctc cct ctg ttt cgg gac tgg atc aaa gag aac act 2581
 Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr
 225 230 235

ggg gta tag gggccggggc caccctaaatg tgtacacctg cggggccacc 2630
 Gly Val *
 240

catcgtccac cccagtgtgc acgcctgcag gctggagact ggaccgctga ctgcaccagc 2690
 gccccagaa catacactgt gaactcaatc tccagggctc caaatctgcc tagaaaacct 2750
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 aacaatttat ttctttttta aaaaaaaaaa aaaaaaa 3147

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 <211> 241
 <212> PRT
 <213> Homo Sapien

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 20 25 30
 Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
 35 40 45
 Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
 50 55 60
 His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
 65 70 75 80
 Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
 85 90 95
 Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
 100 105 110
 Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
 115 120 125
 Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
 130 135 140
 Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
 145 150 155 160
 Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
 165 170 175
 Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
 180 185 190
 Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
 195 200 205
 Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
 210 215 220
 Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
 225 230 235 240
 Val

<210> 51
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleoide Primer

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 <210> 52
 <211> 43
 <212> DNA
 <213> Aritificial sequence

 <400> 52
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 <210> 53
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleoide Primer

 <400> 53
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 <210> 54
 <211> 43
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleoide Primer

 <400> 54
 ggcacagtca ggcccatctc tctgcccttc tttgatgagg agc 43

 <210> 55
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 <212> DNA
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 <220>
 <223> Oligonucleoide Primer

 <400> 55
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 <220>
 <223> Oligonucleoide Primer

 <400> 56
 tacctctcct acgactcc 18

 <210> 57
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide Primer

<400> 57
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<210> 58
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 58
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<210> 59
 <211> 11
 <212> PRT
 <213> Homo Sapien

<400> 59
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 1 5 10

<210> 60
 <211> 32
 <212> PRT
 <213> Homo Sapien

<400> 60
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 1 5 10 15
 Leu Cys Trp Arg Lys Pro Thr Lys Met Lys Gly Pro Arg Pro Ser His
 20 25 30

<210> 61
 <211> 4933
 <212> DNA
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<220>
 <221> CDS
 <222> (94)...(3222)
 <223> Nucleotide sequence encoding corin

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 <309> 1999-05-24

<400> 61
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 Met Lys Gln Ser Pro Ala Leu
 1 5

gct ccg gaa gag cgc tac cgc aga gcc ggg tcc cca aag ccg gtc ttg 162
 Ala Pro Glu Glu Arg Tyr Arg Arg Ala Gly Ser Pro Lys Pro Val Leu
 10 15 20

aga gct gat gac aat aac atg ggc aat ggc tgc tct cag aag ctg gcg 210

Arg	Ala	Asp	Asp	Asn	Asn	Met	Gly	Asn	Gly	Cys	Ser	Gln	Lys	Leu	Ala		
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act	gct	aac	ctc	ctc	cgg	ttc	cta	ttg	ctg	gtc	ctg	att	cca	tgt	atc	258	
Thr	Ala	Asn	Leu	Leu	Arg	Phe	Leu	Leu	Leu	Val	Leu	Ile	Pro	Cys	Ile	55	
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tgt	gct	ctc	gtt	ctc	ttg	ctg	gtg	atc	ctg	ctt	tcc	tat	gtt	gga	aca	306	
Cys	Ala	Leu	Val	Leu	Leu	Leu	Val	Ile	Leu	Leu	Ser	Tyr	Val	Gly	Thr	70	
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Leu	Gln	Lys	Val	Tyr	Phe	Lys	Ser	Asn	Gly	Ser	Glu	Pro	Leu	Val	Thr	85	
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gat	ggg	gaa	atc	caa	ggg	tcc	gat	gtt	att	ctt	aca	aat	aca	att	tat	402	
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Asn	Gln	Ser	Thr	Val	Val	Ser	Thr	Ala	His	Pro	Asp	Gln	His	Val	Pro	115	
	105					110											
gcc	tgg	act	acg	gat	gct	tct	ctc	cca	ggg	gac	caa	agt	cac	agg	aat	498	
Ala	Trp	Thr	Thr	Asp	Ala	Ser	Leu	Pro	Gly	Asp	Gln	Ser	His	Arg	Asn	135	
120					125				130								
aca	agt	gcc	tgt	atg	aac	atc	acc	cac	agc	cag	tgt	cag	atg	ctg	ccc	546	
Thr	Ser	Ala	Cys	Met	Asn	Ile	Thr	His	Ser	Gln	Cys	Gln	Met	Leu	Pro	150	
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Tyr	His	Ala	Thr	Leu	Thr	Pro	Leu	Leu	Ser	Val	Val	Arg	Asn	Met	Glu	165	
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Met	Glu	Lys	Phe	Leu	Lys	Phe	Phe	Thr	Tyr	Leu	His	Arg	Leu	Ser	Cys	180	
		170				175											
tat	caa	cat	atc	atg	ctg	ttt	ggc	tgt	acc	ctc	gcc	ttc	cct	gag	tgc	690	
Tyr	Gln	His	Ile	Met	Leu	Phe	Gly	Cys	Thr	Leu	Ala	Phe	Pro	Glu	Cys	195	
	185					190											
atc	att	gat	ggc	gat	gac	agt	cat	gga	ctc	ctg	ccc	tgt	agg	tcc	ttc	738	
Ile	Ile	Asp	Gly	Asp	Asp	Ser	His	Gly	Leu	Leu	Pro	Cys	Arg	Ser	Phe	215	
200					205					210							
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Cys	Glu	Ala	Ala	Lys	Glu	Gly	Cys	Glu	Ser	Val	Leu	Gly	Met	Val	Asn	230	
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Tyr	Ser	Trp	Pro	Asp	Phe	Leu	Arg	Cys	Ser	Gln	Phe	Arg	Asn	Gln	Thr	245	
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	265					270											

gga atc tgc atc ccc ggg aaa ctg caa tgt aat ggc tac aac gac tgt	978
Gly Ile Cys Ile Pro Gly Lys Leu Gln Cys Asn Gly Tyr Asn Asp Cys	
280 285 290 295	
gac gac tgg agt gac gag gct cat tgc aac tgc agc gag aat ctg ttt	1026
Asp Asp Trp Ser Asp Glu Ala His Cys Asn Cys Ser Glu Asn Leu Phe	
300 305 310	
cac tgt cac aca ggc aag tgc ctt aat tac agc ctt gtg tgt gat gga	1074
His Cys His Thr Gly Lys Cys Leu Asn Tyr Ser Leu Val Cys Asp Gly	
315 320 325	
tat gat gac tgt ggg gat ttg agt gat gag caa aac tgt gat tgc aat	1122
Tyr Asp Asp Cys Gly Asp Leu Ser Asp Glu Gln Asn Cys Asp Cys Asn	
330 335 340	
ccc aca aca gag cat cgc tgc ggg gac ggg cgc tgc atc gcc atg gag	1170
Pro Thr Thr Glu His Arg Cys Gly Asp Gly Arg Cys Ile Ala Met Glu	
345 350 355	
tgg gtg tgt gat ggt gac cac gac tgt gtg gat aag tcc gac gag gtc	1218
Trp Val Cys Asp Gly Asp His Asp Cys Val Asp Lys Ser Asp Glu Val	
360 365 370 375	
aac tgc tcc tgt cac agc cag ggt ctg gtg gaa tgc aga aat gga caa	1266
Asn Cys Ser Cys His Ser Gln Gly Leu Val Glu Cys Arg Asn Gly Gln	
380 385 390	
tgt atc ccc agc acg ttt caa tgt gat ggt gac gag gac tgc aag gat	1314
Cys Ile Pro Ser Thr Phe Gln Cys Asp Gly Asp Glu Asp Cys Lys Asp	
395 400 405	
ggg agt gat gag gag aac tgc agc gtc att cag act tca tgt caa gaa	1362
Gly Ser Asp Glu Glu Asn Cys Ser Val Ile Gln Thr Ser Cys Gln Glu	
410 415 420	
gga gac caa aga tgc ctc tac aat ccc tgc ctt gat tca tgt ggt ggt	1410
Gly Asp Gln Arg Cys Leu Tyr Asn Pro Cys Leu Asp Ser Cys Gly Gly	
425 430 435	
agc tct ctc tgt gac ccg aac aac agt ctg aat aac tgt agt caa tgt	1458
Ser Ser Leu Cys Asp Pro Asn Asn Ser Leu Asn Asn Cys Ser Gln Cys	
440 445 450 455	
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Glu Pro Ile Thr Leu Glu Leu Cys Met Asn Leu Pro Tyr Asn Ser Thr	
460 465 470	
agt tat cca aat tat ttt ggc cac agg act caa aag gaa gca tcc atc	1554
Ser Tyr Pro Asn Tyr Phe Gly His Arg Thr Gln Lys Glu Ala Ser Ile	
475 480 485	
agc tgg gag tct tct ctt ttc cct gca ctt gtt caa acc aac tgt tat	1602
Ser Trp Glu Ser Ser Leu Phe Pro Ala Leu Val Gln Thr Asn Cys Tyr	
490 495 500	
aaa tac ctc atg ttc ttt tct tgc acc att ttg gta cca aaa tgt gat	1650
Lys Tyr Leu Met Phe Phe Ser Cys Thr Ile Leu Val Pro Lys Cys Asp	
505 510 515	
gtg aat aca ggc gag cgt atc cct cct tgc agg gca ttg tgt gaa cac	1698

Val 520	Asn	Thr	Gly	Glu	Arg 525	Ile	Pro	Pro	Cys	Arg 530	Ala	Leu	Cys	Glu	His 535	
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cct Pro	gaa Glu	gac Asp	aca Thr 555	gat Asp	tgc Cys	agt Ser	caa Gln	ttt Phe 560	cca Pro	gag Glu	gaa Glu	aat Asn	tca Ser 565	gac Asp	aat Asn	1794
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 50 55 60
 Leu Leu Ser Tyr Val Gly Thr Leu Gln Lys Val Tyr Phe Lys Ser Asn
 65 70 75 80
 Gly Ser Glu Pro Leu Val Thr Asp Gly Glu Ile Gln Gly Ser Asp Val
 85 90 95
 Ile Leu Thr Asn Thr Ile Tyr Asn Gln Ser Thr Val Val Ser Thr Ala
 100 105 110
 His Pro Asp Gln His Val Pro Ala Trp Thr Thr Asp Ala Ser Leu Pro
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 Gly Asp Gln Ser His Arg Asn Thr Ser Ala Cys Met Asn Ile Thr His
 130 135 140
 Ser Gln Cys Gln Met Leu Pro Tyr His Ala Thr Leu Thr Pro Leu Leu


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Cys Val Thr Leu Ser Ile Asn Val Asn Ser Ser Ser Phe Leu Met Val
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His Arg Ala Ala Thr Glu His His Val Cys Ala Asp Gly Trp Gln Glu
705      710      715      720
Ile Leu Ser Gln Leu Ala Cys Lys Gln Met Gly Leu Gly Glu Pro Ser
      725      730      735
Val Thr Lys Leu Ile Gln Glu Gln Glu Lys Glu Pro Arg Trp Leu Thr
740      745      750
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      755      760      765
Leu Val Asn Gly Gln Ser Cys Glu Ser Arg Ser Lys Ile Ser Leu Leu
770      775      780
Cys Thr Lys Gln Asp Cys Gly Arg Arg Pro Ala Ala Arg Met Asn Lys
785      790      795      800
Arg Ile Leu Gly Gly Arg Thr Ser Arg Pro Gly Arg Trp Pro Trp Gln
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Cys Ser Leu Gln Ser Glu Pro Ser Gly His Ile Cys Gly Cys Val Leu
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His Pro Ser Val Phe Met Gln Thr Arg Phe Val Lys Thr Ile Ile Leu
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His Pro Arg Tyr Ser Arg Ala Val Val Asp Tyr Asp Ile Ser Ile Val
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Asp Lys Leu Thr Thr Ser His Leu Ala Thr Pro Gly Asn Val Ser					
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ggc Gly	cga Arg	ctg Leu	ctc Leu	tgc Cys	ggc Gly	gca Ala	tct Ser	ctc Leu	gtc Val	agc Ser	agt Ser	gac Asp	tgg Trp	ctg Leu	gtg Val	2503
tcc Ser	gcc Ala	gca Ala	cac His	tgc Cys	gtg Val	tat Tyr	ggg Gly	aga Arg	aac Asn	tta Leu	gag Glu	cca Pro	tcc Ser	aag Lys	tgg Trp	2551
aca Thr	gca Ala	atc Ile	cta Leu	ggc Gly	ctg Leu	cat His	atg Met	aaa Lys	tca Ser	aat Asn	ctg Leu	acc Thr	tct Ser	cct Pro	caa Gln	2599
aca Thr	gtc Val	cct Pro	cga Arg	tta Leu	ata Ile	gat Asp	gaa Glu	att Ile	gtc Val	ata Ile	aac Asn	cct Pro	cat His	tac Tyr	aat Asn	2647
agg Arg	cga Arg	aga Arg	aag Lys	gac Asp	aac Asn	gac Asp	att Ile	gcc Ala	atg Met	atg Met	cat His	ctg Leu	gaa Glu	ttt Phe	aaa Lys	2695
gtg Val	aat Asn	tac Tyr	aca Thr	gat Asp	tac Tyr	ata Ile	caa Gln	cct Pro	att Ile	tgt Cys	tta Leu	ccg Pro	gaa Glu	gaa Glu	aat Asn	2743
caa Gln	gtt Val	ttt Phe	cct Pro	cca Pro	gga Gly	aga Arg	aat Asn	tgt Cys	tct Ser	att Ile	gct Ala	ggg Gly	tgg Trp	ggg Gly	acg Thr	2791
gtt Val	gta Val	tat Tyr	caa Gln	ggg Gly	act Thr	act Thr	gca Ala	aac Asn	ata Ile	ttg Leu	caa Gln	gaa Glu	gct Ala	gat Asp	gtt Val	2839
cct Pro	ctt Leu	cta Leu	tca Ser	aat Asn	gag Glu	aga Arg	tgc Cys	caa Gln	cag Gln	cag Gln	atg Met	cca Pro	gaa Glu	tat Tyr	aac Asn	2887
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agg tgg ttc ctt gct ggt gtg acc tca ttt gga tac aag tgt gcc ctg 3031
 Arg Trp Phe Leu Ala Gly Val Thr Ser Phe Gly Tyr Lys Cys Ala Leu
 985 990 995

cct aat cgc ccc gga gtg tat gcc agg gtc tca agg ttt acc gaa tgg 3079
 Pro Asn Arg Pro Gly Val Tyr Ala Arg Val Ser Arg Phe Thr Glu Trp
 1000 1005 1010

ata caa agt ttt cta cat tag cgcatttctt aaactaaaca ggaaagtgcg 3130
 Ile Gln Ser Phe Leu His *
 1015

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 aaaagttacc aaagggtttt attcttacct atgtcaatga aatgctaggg ggccagggaa 3250
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 35 40 45
 Gly Ala Ala Leu Gly Gln Ser His Glu Ala Arg Ala Thr Phe Lys Ile
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 Thr Ser Gly Val Thr Tyr Asn Pro Asn Leu Gln Asp Lys Leu Ser Val
 65 70 75 80
 Asp Phe Lys Val Leu Ala Phe Asp Leu Gln Gln Met Ile Asp Glu Ile
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 Phe Leu Ser Ser Asn Leu Lys Asn Glu Tyr Lys Asn Ser Arg Val Leu
 100 105 110
 Gln Phe Glu Asn Gly Ser Ile Ile Val Val Phe Asp Leu Phe Phe Ala
 115 120 125
 Gln Trp Val Ser Asp Gln Asn Val Lys Glu Glu Leu Ile Gln Gly Leu
 130 135 140
 Glu Ala Asn Lys Ser Ser Gln Leu Val Thr Phe His Ile Asp Leu Asn
 145 150 155 160
 Ser Val Asp Ile Leu Asp Lys Leu Thr Thr Ser His Leu Ala Thr
 165 170 175
 Pro Gly Asn Val Ser Ile Glu Cys Leu Pro Gly Ser Ser Pro Cys Thr
 180 185 190
 Asp Ala Leu Thr Cys Ile Lys Ala Asp Leu Phe Cys Asp Gly Glu Val
 195 200 205
 Asn Cys Pro Asp Gly Ser Asp Glu Asp Asn Lys Met Cys Ala Thr Val
 210 215 220

Cys Asp Gly Arg Phe Leu Leu Thr Gly Ser Ser Gly Ser Phe Gln Ala
 225 230 235 240
 Thr His Tyr Pro Lys Pro Ser Glu Thr Ser Val Val Cys Gln Trp Ile
 245 250 255
 Ile Arg Val Asn Gln Gly Leu Ser Ile Lys Leu Ser Phe Asp Asp Phe
 260 265 270
 Asn Thr Tyr Tyr Thr Asp Ile Leu Asp Ile Tyr Glu Gly Val Gly Ser
 275 280 285
 Ser Lys Ile Leu Arg Ala Ser Ile Trp Glu Thr Asn Pro Gly Thr Ile
 290 295 300
 Arg Ile Phe Ser Asn Gln Val Thr Ala Thr Phe Leu Ile Glu Ser Asp
 305 310 315 320
 Glu Ser Asp Tyr Val Gly Phe Asn Ala Thr Tyr Thr Ala Phe Asn Ser
 325 330 335
 Ser Glu Leu Asn Asn Tyr Glu Lys Ile Asn Cys Asn Phe Glu Asp Gly
 340 345 350
 Phe Cys Phe Trp Val Gln Asp Leu Asn Asp Asp Asn Glu Trp Glu Arg
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 Ile Gln Gly Ser Thr Phe Ser Pro Phe Thr Gly Pro Asn Phe Asp His
 370 375 380
 Thr Phe Gly Asn Ala Ser Gly Phe Tyr Ile Ser Thr Pro Thr Gly Pro
 385 390 395 400
 Gly Gly Arg Gln Glu Arg Val Gly Leu Leu Ser Leu Pro Leu Asp Pro
 405 410 415
 Thr Leu Glu Pro Ala Cys Leu Ser Phe Trp Tyr His Met Tyr Gly Glu
 420 425 430
 Asn Val His Lys Leu Ser Ile Asn Ile Ser Asn Asp Gln Asn Met Glu
 435 440 445
 Lys Thr Val Phe Gln Lys Glu Gly Asn Tyr Gly Asp Asn Trp Asn Tyr
 450 455 460
 Gly Gln Val Thr Leu Asn Glu Thr Val Lys Phe Lys Val Ala Phe Asn
 465 470 475 480
 Ala Phe Lys Asn Lys Ile Leu Ser Asp Ile Ala Leu Asp Asp Ile Ser
 485 490 495
 Leu Thr Tyr Gly Ile Cys Asn Gly Ser Leu Tyr Pro Glu Pro Thr Leu
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 Val Pro Thr Pro Pro Glu Leu Pro Thr Asp Cys Gly Gly Pro Phe
 515 520 525
 Glu Leu Trp Glu Pro Asn Thr Thr Phe Ser Ser Thr Asn Phe Pro Asn
 530 535 540
 Ser Tyr Pro Asn Leu Ala Phe Cys Val Trp Ile Leu Asn Ala Gln Lys
 545 550 555 560
 Gly Lys Asn Ile Gln Leu His Phe Gln Glu Phe Asp Leu Glu Asn Ile
 565 570 575
 Asn Asp Val Val Glu Ile Arg Asp Gly Glu Glu Ala Asp Ser Leu Leu
 580 585 590
 Leu Ala Val Tyr Thr Gly Pro Gly Pro Val Lys Asp Val Phe Ser Thr
 595 600 605
 Thr Asn Arg Met Thr Val Leu Leu Ile Thr Asn Asp Val Leu Ala Arg
 610 615 620
 Gly Gly Phe Lys Ala Asn Phe Thr Thr Gly Tyr His Leu Gly Ile Pro
 625 630 635 640
 Glu Pro Cys Lys Ala Asp His Phe Gln Cys Lys Asn Gly Glu Cys Val
 645 650 655
 Pro Leu Val Asn Leu Cys Asp Gly His Leu His Cys Glu Asp Gly Ser
 660 665 670
 Asp Glu Ala Asp Cys Val Arg Phe Phe Asn Gly Thr Thr Asn Asn Asn
 675 680 685
 Gly Leu Val Arg Phe Arg Ile Gln Ser Ile Trp His Thr Ala Cys Ala
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Thr	Ile	Ala	Leu	Leu	Val	Tyr	Phe	Leu	Ala	Phe	Asp	Gln	Lys	Ser	Tyr															
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Phe	Tyr	Arg	Ser	Ser	Phe	Gln	Leu	Leu	Asn	Val	Glu	Tyr	Asn	Ser	Gln															
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gaa	tct	ctg	att	act	aaa	aca	ttc	aaa	gaa	tca	aat	tta	aga	aat	cag	349														
Glu	Ser	Leu	Ile	Thr	Lys	Thr	Phe	Lys	Glu	Ser	Asn	Leu	Arg	Asn	Gln															
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ttc	atc	aga	gct	cat	gtt	gcc	aaa	ctg	agg	caa	gat	ggg	agt	ggg	gtg	397														
Phe	Ile	Arg	Ala	His	Val	Ala	Lys	Leu	Arg	Gln	Asp	Gly	Ser	Gly	Val															
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aga	gcg	gat	gtt	gtc	atg	aaa	ttt	caa	ttc	act	aga	aat	aac	aat	gga	445														
Arg	Ala	Asp	Val	Val	Met	Lys	Phe	Gln	Phe	Thr	Arg	Asn	Asn	Asn	Gly															
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Pro	Asp	Leu	Ile	Thr	Leu	Ser	Glu	Gln	Arg	Ile	Leu	Gly	Gly	Thr	Glu															
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 275 280 285

cat agt gtg tgt ctc cca gct gct acc cag aat att cca cct ggc tct 973
 His Ser Val Cys Leu Pro Ala Ala Thr Gln Asn Ile Pro Pro Gly Ser
 290 295 300

act gct tat gta aca gga tgg ggc gct caa gaa tat gct ggc cac aca 1021
 Thr Ala Tyr Val Thr Gly Trp Gly Ala Gln Glu Tyr Ala Gly His Thr
 305 310 315 320

gtt cca gag cta agg caa gga cag gtc aga ata ata agt aat gat gta 1069
 Val Pro Glu Leu Arg Gln Gly Gln Val Arg Ile Ile Ser Asn Asp Val
 325 330 335

tgt aat gca cca cat agt tat aat gga gcc atc ttg tct gga atg ctg 1117
 Cys Asn Ala Pro His Ser Tyr Asn Gly Ala Ile Leu Ser Gly Met Leu
 340 345 350

tgt gct gga gta cct caa ggt gga gtg gac gca tgt cag ggt gac tct 1165
 Cys Ala Gly Val Pro Gln Gly Gly Val Asp Ala Cys Gln Gly Asp Ser
 355 360 365

ggt ggc cca cta gta caa gaa gac tca cgg cgg ctt tgg ttt att gtg 1213
 Gly Gly Pro Leu Val Gln Glu Asp Ser Arg Arg Leu Trp Phe Ile Val
 370 375 380

ggg ata gta agc tgg gga gat cag tgt ggc ctg ccg gat aag cca gga 1261
 Gly Ile Val Ser Trp Gly Asp Gln Cys Gly Leu Pro Asp Lys Pro Gly
 385 390 395 400

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 405 410 415

ggg atc tag tgcaacaagt gcacccctgt tgcaaagtct gtatgcaggt 1358
 Gly Ile *

gtgcctgtct taaattccaa agctttacat ttcaactgaa aaagaaacta gaaatgtcct 1418
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 <213> Homo Sapien

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 35 40 45
 Phe Tyr Arg Ser Ser Phe Gln Leu Leu Asn Val Glu Tyr Asn Ser Gln
 50 55 60
 Leu Asn Ser Pro Ala Thr Gln Glu Tyr Arg Thr Leu Ser Gly Arg Ile
 65 70 75 80
 Glu Ser Leu Ile Thr Lys Thr Phe Lys Glu Ser Asn Leu Arg Asn Gln
 85 90 95

Phe Ile Arg Ala His Val Ala Lys Leu Arg Gln Asp Gly Ser Gly Val
 100 105 110
 Arg Ala Asp Val Val Met Lys Phe Gln Phe Thr Arg Asn Asn Asn Gly
 115 120 125
 Ala Ser Met Lys Ser Arg Ile Glu Ser Val Leu Arg Gln Met Leu Asn
 130 135 140
 Asn Ser Gly Asn Leu Glu Ile Asn Pro Ser Thr Glu Ile Thr Ser Leu
 145 150 155 160
 Thr Asp Gln Ala Ala Asn Trp Leu Ile Asn Glu Cys Gly Ala Gly
 165 170 175
 Pro Asp Leu Ile Thr Leu Ser Glu Gln Arg Ile Leu Gly Gly Thr Glu
 180 185 190
 Ala Glu Glu Gly Ser Trp Pro Trp Gln Val Ser Leu Arg Leu Asn Asn
 195 200 205
 Ala His Cys Gly Gly Ser Leu Ile Asn Asn Met Trp Ile Leu Thr
 210 215 220
 Ala Ala His Cys Phe Arg Ser Asn Ser Asn Pro Arg Asp Trp Ile Ala
 225 230 235 240
 Thr Ser Gly Ile Ser Thr Thr Phe Pro Lys Leu Arg Met Arg Val Arg
 245 250 255
 Asn Ile Leu Ile His Asn Asn Tyr Lys Ser Ala Thr His Glu Asn Asp
 260 265 270
 Ile Ala Leu Val Arg Leu Glu Asn Ser Val Thr Phe Thr Lys Asp Ile
 275 280 285
 His Ser Val Cys Leu Pro Ala Ala Thr Gln Asn Ile Pro Pro Gly Ser
 290 295 300
 Thr Ala Tyr Val Thr Gly Trp Gly Ala Gln Glu Tyr Ala Gly His Thr
 305 310 315 320
 Val Pro Glu Leu Arg Gln Gly Gln Val Arg Ile Ile Ser Asn Asp Val
 325 330 335
 Cys Asn Ala Pro His Ser Tyr Asn Gly Ala Ile Leu Ser Gly Met Leu
 340 345 350
 Cys Ala Gly Val Pro Gln Gly Gly Val Asp Ala Cys Gln Gly Asp Ser
 355 360 365
 Gly Gly Pro Leu Val Gln Glu Asp Ser Arg Arg Leu Trp Phe Ile Val
 370 375 380
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 Gly Ile

<210> 67
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 <223> Nucleotide sequence encoding human hepsin

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 <309> 1993-06-11

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 tggacccag ggtcccaccc tggcccagga ggctagccag ggaatcatta acaagaggca 240

gtgac atg gcg cag aag gag ggt ggc cgg act gtg cca tgc tgc tcc aga 290
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 Pro Lys Val Ala Ala Leu Thr Ala Gly Thr Leu Leu Leu Leu Thr Ala
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 Ile Gly Ala Ala Ser Trp Ala Ile Val Ala Val Leu Leu Arg Ser Asp
 35 40 45

cag gag ccg ctg tac cca gtg cag gtc agc tct gcg gac gct cgg ctc 434
 Gln Glu Pro Leu Tyr Pro Val Gln Val Ser Ser Ala Asp Ala Arg Leu
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atg gtc ttt gac aag acg gaa ggg acg tgg cgg ctg ctg tgc tcc tcg 482
 Met Val Phe Asp Lys Thr Glu Gly Thr Trp Arg Leu Leu Cys Ser Ser
 65 70 75

cgc tcc aac gcc agg gta gcc gga ctc agc tgc gag gag atg ggc ttc 530
 Arg Ser Asn Ala Arg Val Ala Gly Leu Ser Cys Glu Glu Met Gly Phe
 80 85 90 95

ctc agg gca ctg acc cac tcc gag ctg gac gtg cga acg gcg ggc gcc 578
 Leu Arg Ala Leu Thr His Ser Glu Leu Asp Val Arg Thr Ala Gly Ala
 100 105 110

aat ggc acg tcg ggc ttc ttc tgt gtg gac gag ggg agg ctg ccc cac 626
 Asn Gly Thr Ser Gly Phe Phe Cys Val Asp Glu Gly Arg Leu Pro His
 115 120 125

acc cag agg ctg ctg gag gtc atc tcc gtg tgt gat tgc ccc aga ggc 674
 Thr Gln Arg Leu Leu Glu Val Ile Ser Val Cys Asp Cys Pro Arg Gly
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cgt ttc ttg gcc gcc atc tgc caa gac tgt ggc cgc agg aag ctg ccc 722
 Arg Phe Leu Ala Ala Ile Cys Gln Asp Cys Gly Arg Arg Lys Leu Pro
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gtg gac cgc atc gtg gga ggc cgg gac acc agc ttg ggc cgg tgg ccg 770
 Val Asp Arg Ile Val Gly Gly Arg Asp Thr Ser Leu Gly Arg Trp Pro
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tgg caa gtc agc ctt cgc tat gat gga gca cac ctc tgt ggg gga tcc 818
 Trp Gln Val Ser Leu Arg Tyr Asp Gly Ala His Leu Cys Gly Gly Ser
 180 185 190

ctg ctc tcc ggg gac tgg gtg ctg aca gcc gcc cac tgc ttc ccg gag 866
 Leu Leu Ser Gly Asp Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu
 195 200 205

cgg aac cgg gtc ctg tcc cga tgg cga gtg ttt gcc ggt gcc gtg gcc 914
 Arg Asn Arg Val Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala
 210 215 220

cag gcc tct ccc cac ggt ctg cag ctg ggg gtg cag gct gtg gtc tac 962
 Gln Ala Ser Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr
 225 230 235

cac ggg ggc tat ctt ccc ttt cgg gac ccc aac agc gag gag aac agc 1010
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Gly Ala Ala Ser Trp Ala Ile Val Ala Val Leu Leu Arg Ser Asp Gln
 35 40 45
 Glu Pro Leu Tyr Pro Val Gln Val Ser Ser Ala Asp Ala Arg Leu Met
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 Val Phe Asp Lys Thr Glu Gly Thr Trp Arg Leu Leu Cys Ser Ser Arg
 65 70 75 80
 Ser Asn Ala Arg Val Ala Gly Leu Ser Cys Glu Glu Met Gly Phe Leu
 85 90 95
 Arg Ala Leu Thr His Ser Glu Leu Asp Val Arg Thr Ala Gly Ala Asn
 100 105 110
 Gly Thr Ser Gly Phe Phe Cys Val Asp Glu Gly Arg Leu Pro His Thr
 115 120 125
 Gln Arg Leu Leu Glu Val Ile Ser Val Cys Asp Cys Pro Arg Gly Arg
 130 135 140
 Phe Leu Ala Ala Ile Cys Gln Asp Cys Gly Arg Arg Lys Leu Pro Val
 145 150 155 160
 Asp Arg Ile Val Gly Gly Arg Asp Thr Ser Leu Gly Arg Trp Pro Trp
 165 170 175
 Gln Val Ser Leu Arg Tyr Asp Gly Ala His Leu Cys Gly Gly Ser Leu
 180 185 190
 Leu Ser Gly Asp Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg
 195 200 205
 Asn Arg Val Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala Gln
 210 215 220
 Ala Ser Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr His
 225 230 235 240
 Gly Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser Asn
 245 250 255
 Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Glu Tyr
 260 265 270
 Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln Ala Leu Val Asp Gly
 275 280 285
 Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Tyr Tyr Gly Gln
 290 295 300
 Gln Ala Gly Val Leu Gln Glu Ala Arg Val Pro Ile Ile Ser Asn Asp
 305 310 315 320
 Val Cys Asn Gly Ala Asp Phe Tyr Gly Asn Gln Ile Lys Pro Lys Met
 325 330 335
 Phe Cys Ala Gly Tyr Pro Glu Gly Gly Ile Asp Ala Cys Gln Gly Asp
 340 345 350
 Ser Gly Gly Pro Phe Val Cys Glu Asp Ser Ile Ser Arg Thr Pro Arg
 355 360 365
 Trp Arg Leu Cys Gly Ile Val Ser Trp Gly Thr Gly Cys Ala Leu Ala
 370 375 380
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 385 390 395 400
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 405 410 415
 Leu

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<212> DNA

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<221> CDS

<222> (57)...(1535)

<223> Nucleotide sequence encoding human serine protease

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<308> GenBank U75329

<309> 1997-10-10

<400> 69

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His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val Val
                    20                      25                      30

ccc act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg      203
Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro Val
                    35                      40                      45

ccc cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc gtc      251
Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val Val
                    50                      55                      60                      65

tgc acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act      299
Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys Thr
                    70                      75                      80

aag aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga      347
Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val Gly
                    85                      90                      95

gct gcg ctg gcc gct ggc cta ctc tgg aag ttc atg ggc agc aag tgc      395
Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys Cys
                    100                      105                      110

tcc aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc      443
Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn Pro
                    115                      120                      125

tct aac tgg tgt gat ggc gtg tca cac tgc ccc ggc ggg gag gac gag      491
Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu
                    130                      135                      140                      145

aat cgg tgt gtt cgc ctc tac gga cca aac ttc atc ctt cag atg tac      539
Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met Tyr
                    150                      155                      160

tca tct cag agg aag tcc tgg cac cct gtg tgc caa gac gac tgg aac      587
Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp Asn
                    165                      170                      175

gag aac tac ggg ccg gcg gcc tgc agg gac atg ggc tat aag aat aat      635
Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn Asn
                    180                      185                      190

ttt tac tct agc caa gga ata gtg gat gac agc gga tcc acc agc ttt      683
Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser Phe
                    195                      200                      205

atg aaa ctg aac aca agt gcc ggc aat gtc gat atc tat aaa aaa ctg      731
Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys Leu

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210	215	220	225	
tac cac agt gat gcc tgt tct tca aaa gca gtg gtt tct tta cgc tgt				779
Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg Cys	230	235	240	
tta gcc tgc ggg gtc aac ttg aac tca agc cgc cag agc agg atc gtg				827
Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile Val	245	250	255	
ggc ggt gag agc gcg ctc ccg ggg gcc tgg ccc tgg cag gtc agc ctg				875
Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser Leu	260	265	270	
cac gtc cag aac gtc cac gtg tgc gga ggc tcc atc atc acc ccc gag				923
His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro Glu	275	280	285	
tgg atc gtg aca gcc gcc cac tgc gtg gaa aaa cct ctt aac aat cca				971
Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn Pro	290	295	300	305
tgg cat tgg acg gca ttt gcg ggg att ttg aga caa tct ttc atg ttc				1019
Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met Phe	310	315	320	
tat gga gcc gga tac caa gta caa aaa gtg att tct cat cca aat tat				1067
Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Asn Tyr	325	330	335	
gac tcc aag acc aag aac aat gac att gcg ctg atg aag ctg cag aag				1115
Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln Lys	340	345	350	
cct ctg act ttc aac gac cta gtg aaa cca gtg tgt ctg ccc aac cca				1163
Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn Pro	355	360	365	
ggc atg atg ctg cag cca gaa cag ctc tgc tgg att tcc ggg tgg ggg				1211
Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp Gly	370	375	380	385
gcc acc gag gag aaa ggg aag acc tca gaa gtg ctg aac gct gcc aag				1259
Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala Lys	390	395	400	
gtg ctt ctc att gag aca cag aga tgc aac agc aga tat gtc tat gac				1307
Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr Asp	405	410	415	
aac ctg atc aca cca gcc atg atc tgt gcc ggc ttc ctg cag ggg aac				1355
Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly Asn	420	425	430	
gtc gat tct tgc cag ggt gac agt gga ggg cct ctg gtc act tcg aac				1403
Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser Asn	435	440	445	
aac aat atc tgg tgg ctg ata ggg gat aca agc tgg ggt tct ggc tgt				1451
Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly Cys	450	455	460	465

gcc aaa gct tac aga cca gga gtg tac ggg aat gtg atg gta ttc acg 1499
 Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe Thr
 470 475 480

gac tgg att tat cga caa atg aag gca aac ggc taa tccacatggg 1545
 Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly *
 485 490

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 gattttactct tagagatgat tcagaggtca cttcattttt attaaacagt gaacttgtct 1665
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 Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
 35 40 45
 Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
 50 55 60
 Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
 65 70 75 80
 Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
 85 90 95
 Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
 100 105 110
 Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
 115 120 125
 Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
 130 135 140
 Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met
 145 150 155
 Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
 165 170 175
 Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
 180 185 190
 Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
 195 200 205
 Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
 210 215 220
 Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
 225 230 235 240
 Cys Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile

245 250 255
 Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
 260 265 270
 Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Thr Pro
 275 280 285
 Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
 290 295 300
 Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
 305 310 315 320
 Phe Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn
 325 330 335
 Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
 340 345 350
 Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
 355 360 365
 Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
 370 375 380
 Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
 385 390 395 400
 Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
 405 410 415
 Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
 420 425 430
 Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
 435 440 445
 Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
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 gacctgtgtg gggaggccct cctgctgcct tggggtgaca atctcagctc caggctacag 180
 ggagaccggg aggatcacag agccagcatg gtacaggatc ctgacagtga tcaacctctg 240
 aacagcctcg atg tca aac ccc tgc gca aac ccc gta tcc cca tgg aga 289
 Met Ser Asn Pro Cys Ala Asn Pro Val Ser Pro Trp Arg
 1 5 10
 cct tca gaa agt gtg ggg atc ccc atc atc ata gca cta ctg agc ctg 337
 Pro Ser Glu Ser Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu
 15 20 25
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 Ala Ser Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys

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Tyr Tyr Phe Leu Cys 50	Gly Gln Pro Leu His 55	Phe Ile Pro Arg	Lys Gln 60	
ctg tgt gac gga gag ctg gac tgt ccc ttg ggg gag gac gag gag cac				481
Leu Cys Asp Gly 65	Glu Leu Asp Cys Pro 70	Leu Gly Glu Asp	Glu Glu His 75	
tgt gtc aag agc ttc ccc gaa ggg cct gca gtg gca gtc cgc ctc tcc				529
Cys Val Lys 80	Ser Phe Pro Glu Gly 85	Pro Ala Val Ala Val Arg	Leu Ser 90	
aag gac cga tcc aca ctg cag gtg ctg gac tgc gcc aca ggg aac tgg				577
Lys Asp 95	Arg Ser Thr Leu Gln Val Leu Asp 100	Ser Ala Thr Gly Asn	Trp 105	
ttc tct gcc tgt ttc gac aac ttc aca gaa gct ctc gct gag aca gcc				625
Phe Ser Ala Cys Phe 110	Asp Asn Phe Thr Glu Ala 115	Leu Ala Glu Thr	Ala 120	
tgt agg cag atg ggc tac agc agc aaa ccc act ttc aga gct gtg gag				673
Cys Arg Gln Met 130	Tyr Ser Ser Lys 135	Thr Phe Arg Ala Val	Glu 140	
att ggc cca gac cag gat ctg gat gtt gtt gaa atc aca gaa aac agc				721
Ile Gly Pro 145	Asp Gln Asp Leu Asp Val 150	Glu Ile Thr	Asn Ser 155	
cag gag ctt cgc atg cgg aac tca agt ggg ccc tgt ctc tca ggc tcc				769
Gln Glu 160	Leu Arg Met Arg Asn Ser 165	Gly Pro Cys Leu Ser	Gly Ser 170	
ctg gtc tcc ctg cac tgt ctt gcc tgt ggg aag agc ctg aag acc ccc				817
Leu Val Ser Leu His 175	Cys Leu Ala Cys Gly Lys 180	Ser Leu Lys Thr	Pro 185	
cgt gtg gtg ggt ggg gag gag gcc tct gtg gat tct tgg cct tgg cag				865
Arg Val Val Gly 190	Gly Glu Glu Ala Ser Val 195	Asp Ser Trp Pro	Gln 200	
gtc agc atc cag tac gac aaa cag cac gtc tgt gga ggg agc atc ctg				913
Val Ser Ile Gln Tyr 210	Asp Lys Gln His Val 215	Cys Gly Gly Ser	Ile Leu 220	
gac ccc cac tgg gtc ctc acg gca gcc cac tgc ttc agg aaa cat acc				961
Asp Pro His Trp 225	Val Leu Thr Ala Ala His 230	Cys Phe Arg Lys	His Thr 235	
gat gtg ttc aac tgg aag gtg cgg gca ggc tca gac aaa ctg ggc agc				1009
Asp Val Phe Asn Trp 240	Lys Val Arg Ala Gly Ser 245	Asp Lys Leu Gly	Ser 250	
ttc cca tcc ctg gct gtg gcc aag atc atc atc att gaa ttc aac ccc				1057
Phe Pro Ser Leu Ala Val 255	Ala Lys Ile Ile Ile 260	Ile Glu Phe Asn	Pro 265	
atg tac ccc aaa gac aat gac atc gcc ctc atg aag ctg cag ttc cca				1105
Met Tyr Pro Lys Asp 270	Asn Asp Ile Ala Leu Met 275	Lys Leu Gln Phe	Pro 285	

ctc act ttc tca ggc aca gtc agg ccc atc tgt ctg ccc ttc ttt gat 1153
 Leu Thr Phe Ser Gly Thr Val Arg Pro Ile Cys Leu Pro Phe Phe Asp
 290 295 300

gag gag ctc act cca gcc acc cca ctc tgg atc att gga tgg ggc ttt 1201
 Glu Glu Leu Thr Pro Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe
 305 310 315

acg aag cag aat gga ggg aag atg tct gac ata ctg ctg cag gcg tca 1249
 Thr Lys Gln Asn Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser
 320 325 330

gtc cag gtc att gac agc aca cgg tgc aat gca gac gat gcg tac cag 1297
 Val Gln Val Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln
 335 340 345

ggg gaa gtc acc gag aag atg atg tgt gca ggc atc ccg gaa ggg ggt 1345
 Gly Glu Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly
 350 355 360 365

gtg gac acc tgc cag ggt gac agt ggt ggg ccc ctg atg tac caa tct 1393
 Val Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser
 370 375 380

gac cag tgg cat gtg gtg ggc atc gtt agc tgg ggc tat ggc tgc ggg 1441
 Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys Gly
 385 390 395

ggc ccg agc acc cca gga gta tac acc aag gtc tca gcc tat ctc aac 1489
 Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr Leu Asn
 400 405 410

tgg atc tac aat gtc tgg aag gct gag ctg taa tgctgctgcc cctttgcagt 1542
 Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu *
 415 420

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 aaaatgcact gccctactgt tggatatgact accgttacct actgttgtca ttgttattac 2022
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 <213> Homo sapien

<400> 72
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 35 40 45
 Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln Leu Cys Asp
 50 55 60
 Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu His Cys Val Lys
 65 70 75 80

Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg Leu Ser Lys Asp Arg
 85 90 95
 Ser Thr Leu Gln Val Leu Asp Ser Ala Thr Gly Asn Trp Phe Ser Ala
 100 105 110
 Cys Phe Asp Asn Phe Thr Glu Ala Leu Ala Glu Thr Ala Cys Arg Gln
 115 120 125
 Met Gly Tyr Ser Ser Lys Pro Thr Phe Arg Ala Val Glu Ile Gly Pro
 130 135 140
 Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn Ser Gln Glu Leu
 145 150 155 160
 Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser Gly Ser Leu Val Ser
 165 170 175
 Leu His Cys Leu Ala Cys Gly Lys Ser Leu Lys Thr Pro Arg Val Val
 180 185 190
 Gly Gly Glu Glu Ala Ser Val Asp Ser Trp Pro Trp Gln Val Ser Ile
 195 200 205
 Gln Tyr Asp Lys Gln His Val Cys Gly Gly Ser Ile Leu Asp Pro His
 210 215 220
 Trp Val Leu Thr Ala Ala His Cys Phe Arg Lys His Thr Asp Val Phe
 225 230 235 240
 Asn Trp Lys Val Arg Ala Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser
 245 250 255
 Leu Ala Val Ala Lys Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro
 260 265 270
 Lys Asp Asn Asp Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe
 275 280 285
 Ser Gly Thr Val Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu
 290 295 300
 Thr Pro Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln
 305 310 315 320
 Asn Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val
 325 330 335
 Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu Val
 340 345 350
 Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val Asp Thr
 355 360 365
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser Asp Gln Trp
 370 375 380
 His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys Gly Gly Pro Ser
 385 390 395 400
 Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr Leu Asn Trp Ile Tyr
 405 410 415
 Asn Val Trp Lys Ala Glu Leu
 420